GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 10:47:22 ; Search time 1887.56 Seconds
(without alignments)
12516.755 Million cell updates/sec

Title: US-08-956-991-1
Perfect score: 6604
Sequence: 1 tgactgaggccggagcacgg.....gaaaattgccaaaatatatt 6604

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl1:*
9: gb_pl2:*
10: gb_pr1:*
11: gb_pr2:*
12: gb_pr3:*
13: gb_ro:*
14: gb_st:*
15: gb_sy:*
16: gb_un:*
17: gb_vi:*
18: gb_htg:*
19: em_ba:*
20: em_fun:*
21: em_hum1:*
22: em_hum2:*
23: em_in:*
24: em_om:*
25: em_or:*
26: em_ov:*
27: em_pat:*
28: em_ph:*
29: em_pl:*
30: em_ro:*
31: em_sy:*
32: em_un:*
33: em_vi:*
34: em_htg:*
35: em_sts:*
36: gb_ba1:*
37: gb_ba2:*
38: gb_sts:*
39: gb_pl1:*
40: gb_pl2:*
41: gb_pr1:*
42: gb_pr2:*
43: gb_pr3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
	1	6212	94.1	6413	11	AF023450	AF023450 Homo sapi
	2	6212	94.1	6413	42	AF023450	AF023450 Homo sapi
	3	6110	92.5	6110	11	AF023449	AF023449 Homo sapi
	4	6110	92.5	6110	42	AF023449	AF023449 Homo sapi
	5	699	10.6	721	11	HUMYZ91F03	AF086100 Homo sapi
	6	699	10.6	721	42	HUMYZ91F03	AF086100 Homo sapi
	7	495.4	7.5	109866	11	AF043945	AF043945 Homo sapi
	8	495.4	7.5	109866	42	AF043945	AF043945 Homo sapi
c	9	358.8	5.4	430	38	G36681	G36681 SHGC-53823
c	10	319.4	4.8	120007	11	AF064864	AF064864 Homo sapi
c	11	319.4	4.8	120007	42	AF064864	AF064864 Homo sapi
c	12	307.2	4.7	155407	11	AF042090	AF042090 Homo sapi
c	13	307.2	4.7	121019	11	AF042091	AF042091 Homo sapi
c	14	307.2	4.7	155407	42	AF042090	AF042090 Homo sapi
c	15	307.2	4.7	121019	42	AF042091	AF042091 Homo sapi
	16	296	4.5	145861	11	AF064862	AF064862 Homo sapi
c	17	296	4.5	159424	11	AF064865	AF064865 Homo sapi
	18	296	4.5	145861	42	AF064862	AF064862 Homo sapi
c	19	296	4.5	159424	42	AF064865	AF064865 Homo sapi
	20	89	1.3	7606	3	DROLARM	M27700 D.melanogas
c	21	78	1.2	331519	18	CEY39B6	Z95399 Caenorhabdi
c	22	75.8	1.1	3252	11	HSTAFII13	Y11354 H.sapiens m
c	23	75.8	1.1	3252	42	HSTAFII13	Y11354 H.sapiens m
c	24	74.8	1.1	135301	17	BHV1CGEN	AJ004801 Bovine he
c	25	74.8	1.1	8113	17	HSBBICP4A	L14320 Bovine herp
	26	73.4	1.1	43058	11	HSGG1	Z84721 Human DNA s
	27	73.4	1.1	2685	11	HUMHBA3	J00184 Human alpha
	28	73.4	1.1	43058	42	HSGG1	Z84721 Human DNA s
	29	73.4	1.1	2685	42	HUMHBA3	J00184 Human alpha
	30	73.2	1.1	200000	18	AC004670	AC004670 *** SEQUE
	31	72	1.1	38939	11	AC004678	AC004678 Homo sapi
	32	72	1.1	8113	17	HSBBICP4A	L14320 Bovine herp
	33	72	1.1	38939	42	AC004678	AC004678 Homo sapi
	34	71.8	1.1	2026	5	GGU47276	U47276 Gallus gall
c	35	71.6	1.1	2764	17	HSBBICP4B	L14321 Bovine herp
	36	70.4	1.1	73	11	HSZ98234	Z98234 H.sapiens D
	37	70.4	1.1	73	42	HSZ98234	Z98234 H.sapiens D
	38	69.6	1.1	3957	6	A45258	A45258 Sequence 2
c	39	69.6	1.1	154746	17	HSV2HG52	Z86099 Herpes simp
	40	68.8	1.0	1560	17	HS2IE	M29384 Herpes simp
c	41	68.2	1.0	42301	12	AC005943	AC005943 Homo sapi
c	42	68.2	1.0	42301	43	AC005943	AC005943 Homo sapi
	43	67.8	1.0	1829	5	S46000	S46000 TGF beta 3=
	44	67.8	1.0	10144	10	HUMHMGIY	L17131 Human high
c	45	67.8	1.0	4233	12	HSU75308	U75308 Human TBP-a

ALIGNMENTS

RESULT 1
AF023450
LOCUS AF023450 6413 bp mRNA PRI 02-JUN-1998
DEFINITION Homo sapiens CHD2-52 Down syndrome cell adhesion molecule (DSCAM) mRNA, complete cds.
ACCESSION AF023450
NID g3169767
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6413)
AUTHORS Yamakawa,K., Huo,Y.-K., Haendel,M.A., Hubert,R., Chen,X.-N., Lyons,G.E. and Korenberg,J.R.
TITLE DSCAM: a Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6413)
AUTHORS Yamakawa,K., Huo,Y.-K., Haendel,M.A., Hubert,R., Chen,X.-N., Lyons,G.E. and Korenberg,J.R.
TITLE Direct Submission

```
                /note="GRAIL, score = 89.000%, comment = excellent shadow"
                /evidence=not_experimental
     exon       151739. .151880
                /note="GRAIL, score = 69.000%, comment = good"
                /evidence=not_experimental
     repeat_region  152536. .152946
                /rpt_family="MLT2FA"
                /evidence=not_experimental
     exon       152953. .153051
                /note="MZEF, score = 67.3%"
                /evidence=not_experimental
     repeat_region  152953. .153254
                /rpt_family="AluYa5"
                /evidence=not_experimental
     repeat_region  153261. .153298
                /rpt_family="MLT2FA"
                /evidence=not_experimental
     exon       complement(153269. .153313)
                /note="MZEF, score = 58.8%"
                /evidence=not_experimental
     repeat_region  complement(153386. .153751)
                /rpt_family="THE1B"
                /evidence=not_experimental
     exon       153485. .153555
                /note="GRAIL, score = 62.000%, comment = good"
                /evidence=not_experimental
     exon       153870. .153969
                /note="MZEF, score = 46.9%"
                /evidence=not_experimental
     exon       153870. .153969
                /note="GRAIL, score = 99.000%, comment = excellent"
                /evidence=not_experimental
     repeat_region  154690. .155296
                /rpt_family="L2"
                /evidence=not_experimental
     exon       complement(154820. .154963)
                /note="MZEF, score = 52.2%"
                /evidence=not_experimental
BASE COUNT    48810 a  30519 c  30142 g  45936 t
ORIGIN


  Query Match             4.7%;  Score 307.2;  DB 42;  Length 155407;
  Best Local Similarity   89.7%;  Pred. No. 2.3e-48;
  Matches  330;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy   1654 tccttgaagatggaactcccaaaattatttctgcctttagtgaaaaggtggtgagtccag 1713
           | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2884 TTCCTGCAGATGGAACTCCCAAAATTATTTCTGCCTTTAGTGAAAAGGTGGTGAGTCCAG 2825

Qy   1714 cagagccggtttcccttatgtgcaacgtgaagggaacacctttgcccacgatcacgtgga 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2824 CAGAGCCGGTTTCCCTTATGTGCAACGTGAAGGGAACACCTTTGCCCACGATCACGTGGA 2765

Qy   1774 ccctggacgatgacccgattctcaagggtggcagtcaccgcatcagccagatgatcacgt 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764 CCCTGGACGATGACCCGATTCTCAAGGGTGGCAGTCACCGCATCAGCCAGATGATCACGT 2705

Qy   1834 cggaggggaacgtggtcagctacctgaacatctccagc cccaggtccgggacg gggag 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704 CGGAGGGGAACGTGGTCAGCTACCTGAACATCTCCAGCTCCCAGGTCCGGGACGGGGGAG 2645

Qy   1894 tctaccgctgcactgccaacaactcggcgggagtcgtcctgtaccaggctcgaataaacg 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2644 TCTACCGCTGCACTGCCAACAACTCGGCGGGAGTCGTCCTGTACCAGGCTCGAATAAACG 2585

Qy   1954 taagagggcctgcaagcattcgaccaatgaaaaacatcacagcaatagcaggacgggaca 2013
           ||||||| ||      || | |    ||||  |||| | |     | ||| |
Db   2584 TAAGAGGTGCTTGTCAAATCAGCTCCTCAAAAAAACACACATAACTCATTATAGTGGAGA 2525

Qy   2014 catacatt 2021
             | |||
Db   2524 AGAAGATT 2517
```

```
RESULT  15
AF042091/c
LOCUS       AF042091   121019 bp    DNA             PRI       21-MAR-1998
DEFINITION  Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence.
ACCESSION   AF042091
NID         g2829109
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 121019)
  AUTHORS   Blechschmidt,K., Nordsiek,G., Dagand,E., Hildmann,T., Drescher,B.,
            Weber,J., Schattevoy,R., Rosenthal,A. and Yaspo,M.-L.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1998) Genome Analysis, Institute for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
FEATURES             Location/Qualifiers
     source          1. .121019
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.3"
                     /clone="PAC 267O10"
     repeat_region   325. .1645
                     /rpt_family="CHARLIE1a"
                     /evidence=not_experimental
     exon            complement(518. .541)
                     /note="Xpound exon prediction, score = 65% (0%)"
                     /evidence=not_experimental
     exon            3788. .3962
                     /note="MZEF, score = 82.8%"
                     /evidence=not_experimental
     exon            3895. .3962
                     /note="GRAIL, score = 86.000%, comment = excellent"
                     /evidence=not_experimental
     exon            4383. .4541
                     /note="MZEF, score = 87%"
                     /evidence=not_experimental
     exon            4525. .4541
                     /note="Xpound exon prediction, score = 69% (0%)"
                     /evidence=not_experimental
     repeat_region   complement(4817. .4988)
                     /rpt_family="MIR"
                     /evidence=not_experimental
     repeat_region   complement(5542. .5923)
                     /rpt_family="L1PA12"
                     /evidence=not_experimental
     repeat_region   complement(6481. .8905)
                     /rpt_family="L1MC4"
                     /evidence=not_experimental
     exon            complement(6995. .7113)
                     /note="GRAIL, score = 62.000%, comment = good"
                     /evidence=not_experimental
     exon            complement(7525. .7650)
                     /note="GRAIL, score = 76.000%, comment = excellent"
                     /evidence=not_experimental
     repeat_region   complement(8882. .9257)
                     /rpt_family="L1M4"
                     /evidence=not_experimental
     exon            complement(9253. .9383)
                     /note="GRAIL, score = 66.000%, comment = good"
                     /evidence=not_experimental
     repeat_region   complement(9296. .9595)
                     /rpt_family="L1"
                     /evidence=not_experimental
     repeat_region   complement(9585. .9685)
                     /rpt_family="L1M4"
                     /evidence=not_experimental
     repeat_region   complement(9807. .9857)
                     /rpt_family="L1M4"
```

```
                /evidence=not_experimental
repeat_region   complement(9974. .10289)
                /rpt_family="L1M4"
                /evidence=not_experimental
repeat_region   complement(10290. .10591)
                /rpt_family="AluJb"
                /evidence=not_experimental
exon            10313. .10768
                /note="MZEF, score = 93.1%"
                /evidence=not_experimental
repeat_region   complement(10592. .10666)
                /rpt_family="L1M4"
                /evidence=not_experimental
repeat_region   11825. .11966
                /rpt_family="L1PA13"
                /evidence=not_experimental
repeat_region   13065. .13241
                /rpt_family="MIR"
                /evidence=not_experimental
repeat_region   15010. .15079
                /rpt_family="L2"
                /evidence=not_experimental
exon            complement(15140. .15248)
                /note="Xpound exon prediction, score = 92% (0%)"
                /evidence=not_experimental
exon            complement(15140. .15248)
                /note="GRAIL, score = 80.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   15375. .15571
                /rpt_family="MIR"
                /evidence=not_experimental
repeat_region   complement(15873. .16004)
                /rpt_family="MLT1D"
                /evidence=not_experimental
repeat_region   complement(16013. .16582)
                /rpt_family="L1PA7"
                /evidence=not_experimental
exon            complement(16163. .16311)
                /note="GRAIL, score = 59.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(16583. .16800)
                /rpt_family="MLT1D"
                /evidence=not_experimental
exon            17819. .17973
                /note="GRAIL, score = 52.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   complement(18870. .18957)
                /rpt_family="MER5A"
                /evidence=not_experimental
repeat_region   19091. .19141
                /rpt_family="L2"
                /evidence=not_experimental
exon            complement(19339. .19492)
                /note="GRAIL, score = 86.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(19339. .19492)
                /note="MZEF, score = 89.4%"
                /evidence=not_experimental
repeat_region   19696. .20937
                /rpt_family="L1PA12"
                /evidence=not_experimental
exon            complement(20625. .20660)
                /note="Xpound exon prediction, score = 67% (0%)
                /evidence=not_experimental
exon            22195. .22352
                /note="GRAIL, score = 51.000%, comment = good"
                /evidence=not_experimental
exon            22195. .22340
                /note="MZEF, score = 91.1%"
                /evidence=not_experimental
repeat_region   22277. .22423
                /rpt_family="MER45"
                /evidence=not_experimental
exon            22823. .22898
                /note="GRAIL, score = 81.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   22958. .23259
                /rpt_family="AluSx"
                /evidence=not_experimental
exon            complement(25001. .25141)
                /note="MZEF, score = 59.3%"
                /evidence=not_experimental
repeat_region   25029. .25346
                /rpt_family="AluSx"
                /evidence=not_experimental
exon            complement(25388. .25494)
                /note="GRAIL, score = 70.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   25543. .25618
                /rpt_family="MER81"
                /evidence=not_experimental
repeat_region   complement(25656. .26011)
                /rpt_family="THE1A"
                /evidence=not_experimental
exon            25763. .25858
                /note="GRAIL, score = 62.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(26012. .27563)
                /rpt_family="THE1A-internal"
                /evidence=not_experimental
exon            26952. .26987
                /note="GRAIL, score = 84.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   complement(27564. .27918)
                /rpt_family="THE1A"
                /evidence=not_experimental
exon            complement(27568. .27607)
                /note="GRAIL, score = 68.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   27989. .28342
                /rpt_family="THE1A"
                /evidence=not_experimental
exon            28574. .28644
                /note="GRAIL, score = 91.000%, comment = excellent"
                /evidence=not_experimental
exon            28956. .29064
                /note="GRAIL, score = 64.000%, comment = good"
                /evidence=not_experimental
exon            complement(29675. .29918)
                /note="GRAIL, score = 53.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   30413. .31029
                /rpt_family="MLT1E"
                /evidence=not_experimental
exon            30695. .30757
                /note="GRAIL, score = 77.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   complement(32142. .32294)
                /rpt_family="MER21B"
                /evidence=not_experimental
repeat_region   complement(32266. .32925)
                /rpt_family="MER21B"
                /evidence=not_experimental
repeat_region   33377. .33585
                /rpt_family="LTR16A"
                /evidence=not_experimental
repeat_region   33614. .33664
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   33727. .33869
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   34210. .34419
                /rpt_family="MLT1E"
                /evidence=not_experimental
repeat_region   34555. .34866
```

```
                /rpt_family="MLT1E"
                /evidence=not_experimental
exon            34564. .34803
                /note="MZEF, score = 54.9%"
                /evidence=not_experimental
repeat_region   complement(35138. .35186)
                /rpt_family="MLT2FB"
                /evidence=not_experimental
repeat_region   complement(35262. .35610)
                /rpt_family="MLT2FB"
                /evidence=not_experimental
exon            complement(35356. .35425)
                /note="Xpound exon prediction, score = 86% (0%)"
                /evidence=not_experimental
exon            complement(35526. .35576)
                /note="MZEF, score = 71.6%"
                /evidence=not_experimental
repeat_region   complement(35611. .35757)
                /rpt_family="HERVL"
                /evidence=not_experimental
repeat_region   35918. .36248
                /rpt_family="MER2"
                /evidence=not_experimental
exon            complement(36559. .36616)
                /note="GRAIL, score = 73.000%, comment = good"
                /evidence=not_experimental
exon            complement(36904. .37043)
                /note="GRAIL, score = 84.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   37264. .37851
                /rpt_family="LTR10C"
                /evidence=not_experimental
exon            37342. .37410
                /note="MZEF, score = 57.9%"
                /evidence=not_experimental
exon            complement(37486. .37761)
                /note="GRAIL, score = 57.000%, comment = good"
                /evidence=not_experimental
exon            complement(37531. .37761)
                /note="MZEF, score = 64.3%"
                /evidence=not_experimental
exon            complement(37703. .37761)
                /note="Xpound exon prediction, score = 78% (0%)"
                /evidence=not_experimental
repeat_region   38101. .38163
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   complement(38461. .38815)
                /rpt_family="AluY"
                /evidence=not_experimental
exon            complement(39182. .39306)
                /note="GRAIL, score = 52.000%, comment = good"
                /evidence=not_experimental
repeat_region   39987. .40042
                /rpt_family="MSTC"
                /evidence=not_experimental
repeat_region   40047. .40449
                /rpt_family="MLT2CB"
                /evidence=not_experimental
repeat_region   40536. .40597
                /rpt_family="MLT2CB"
                /evidence=not_experimental
repeat_region   40607. .40791
                /rpt_family="MLT1A2"
                /evidence=not_experimental
repeat_region   40883. .41019
                /rpt_family="MLT1A2"
                /evidence=not_experimental
exon            complement(40950. .40989)
                /note="MZEF, score = 87.7%"
                /evidence=not_experimental
repeat_region   41168. .41299
                /rpt_family="MLT1A2"
                /evidence=not_experimental
exon            41469. .41625
                /note="GRAIL, score = 93.000%, comment = excellent"
                /evidence=not_experimental
exon            41469. .41625
                /note="MZEF, score = 95.9%"
                /evidence=not_experimental
repeat_region   41600. .41660
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   42123. .43695
                /rpt_family="L1PB2"
                /evidence=not_experimental
repeat_region   43706. .44004
                /rpt_family="AluSx"
                /evidence=not_experimental
repeat_region   44005. .45434
                /rpt_family="L1PB2"
                /evidence=not_experimental
repeat_region   45607. .45971
                /rpt_family="L1PB2"
                /evidence=not_experimental
repeat_region   46004. .46379
                /rpt_family="MER7B"
                /evidence=not_experimental
repeat_region   46404. .46702
                /rpt_family="AluSq"
                /evidence=not_experimental
repeat_region   46802. .46930
                /rpt_family="L2"
                /evidence=not_experimental
exon            47384. .47428
                /note="GRAIL, score = 93.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            complement(47438. .47568)
                /note="MZEF, score = 58.5%"
                /evidence=not_experimental
repeat_region   47464. .47657
                /rpt_family="AluSq"
                /evidence=not_experimental
exon            complement(47666. .47773)
                /note="GRAIL, score = 73.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(48310. .48744)
                /rpt_family="MLT1C"
                /evidence=not_experimental
repeat_region   complement(49024. .49125)
                /rpt_family="MLT1C"
                /evidence=not_experimental
repeat_region   49370. .49462
                /rpt_family="MSTA"
                /evidence=not_experimental
exon            49839. .49882
                /note="GRAIL, score = 46.000%, comment = marginal"
                /evidence=not_experimental
repeat_region   50350. .50658
                /rpt_family="MER4A"
                /evidence=not_experimental
repeat_region   50720. .50839
                /rpt_family="MER4C"
                /evidence=not_experimental
exon            51713. .51821
                /note="MZEF, score = 59.3%"
                /evidence=not_experimental
repeat_region   complement(52430. .52777)
                /rpt_family="MLT1A1"
                /evidence=not_experimental
exon            52914. .53206
                /note="GRAIL, score = 54.000%, comment = good"
                /evidence=not_experimental
repeat_region   53832. .54127
                /rpt_family="AluJo"
                /evidence=not_experimental
```

```
exon            complement(54885. .55059)
                /note="Xpound exon prediction, score = 91% (0%)"
                /evidence=not_experimental
exon            complement(54886. .55059)
                /note="MZEF, score = 98.9%"
                /evidence=not_experimental
exon            complement(54886. .55042)
                /note="GRAIL, score = 100.000%, comment = excellent
                shadow"
                /evidence=not_experimental
exon            54948. .55027
                /note="GRAIL, score = 50.000%, comment = good"
                /evidence=not_experimental
exon            55787. .55977
                /note="GRAIL, score = 40.000%, comment = marginal"
                /evidence=not_experimental
repeat_region   56532. .56677
                /rpt_family="AluSg/x"
                /evidence=not_experimental
repeat_region   56684. .57076
                /rpt_family="L1M4"
                /evidence=not_experimental
repeat_region   57078. .57239
                /rpt_family="MER58B"
                /evidence=not_experimental
repeat_region   57240. .57506
                /rpt_family="AluJo"
                /evidence=not_experimental
repeat_region   57651. .57724
                /rpt_family="MER58A"
                /evidence=not_experimental
repeat_region   58130. .58919
                /rpt_family="L1PA8"
                /evidence=not_experimental
repeat_region   complement(58971. .59277)
                /rpt_family="AluJo"
                /evidence=not_experimental
repeat_region   59602. .59969
                /rpt_family="MLT1F"
                /evidence=not_experimental
repeat_region   59971. .60055
                /rpt_family="MIR"
                /evidence=not_experimental
exon            complement(60387. .60438)
                /note="MZEF, score = 73.5%"
                /evidence=not_experimental
repeat_region   complement(60507. .60641)
                /rpt_family="L1MC/D"
                /evidence=not_experimental
repeat_region   61095. .61399
                /rpt_family="AluY"
                /evidence=not_experimental
exon            61096. .61193
                /note="MZEF, score = 75.3%"
                /evidence=not_experimental
exon            complement(62474. .62691)
                /note="GRAIL, score = 53.000%, comment = good"
                /evidence=not_experimental
repeat_region   62475. .62574
                /rpt_family="MIR"
                /evidence=not_experimental
exon            63002. .63139
                /note="MZEF, score = 72.9%"
                /evidence=not_experimental
exon            64197. .64260
                /note="GRAIL, score = 61.000%, comment = good"
                /evidence=not_experimental
exon            64751. .64827
                /note="GRAIL, score = 68.000%, comment = good"
                /evidence=not_experimental
exon            65435. .65566
                /note="GRAIL, score = 49.000%, comment = marginal"
                /evidence=not_experimental
exon            complement(65455. .65742)
                /note="GRAIL, score = 53.000%, comment = good shadow"
                /evidence=not_experimental
exon            complement(65455. .65574)
                /note="Xpound exon prediction, score = 94% (0%)"
                /evidence=not_experimental
exon            65628. .65860
                /note="GRAIL, score = 56.000%, comment = good"
                /evidence=not_experimental
exon            complement(65655. .65750)
                /note="Xpound exon prediction, score = 72% (0%)"
                /evidence=not_experimental
exon            complement(65910. .65984)
                /note="Xpound exon prediction, score = 91% (0%)"
                /evidence=not_experimental
exon            65920. .66014
                /note="GRAIL, score = 54.000%, comment = good"
                /evidence=not_experimental
exon            complement(66074. .66231)
                /note="GRAIL, score = 86.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            complement(66136. .66206)
                /note="Xpound exon prediction, score = 79% (0%)"
                /evidence=not_experimental
exon            complement(66323. .66370)
                /note="GRAIL, score = 53.000%, comment = good shadow"
                /evidence=not_experimental
exon            66961. .67155
                /note="GRAIL, score = 82.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   67057. .67492
                /rpt_family="L1M4"
                /evidence=not_experimental
repeat_region   complement(67522. .67693)
                /rpt_family="MIR"
                /evidence=not_experimental
exon            67981. .68090
                /note="GRAIL, score = 67.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(68260. .68568)
                /rpt_family="MER44A"
                /evidence=not_experimental
repeat_region   69130. .69427
                /rpt_family="AluSg"
                /evidence=not_experimental
repeat_region   69951. .70130
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   70286. .70363
                /rpt_family="L2"
                /evidence=not_experimental
exon            71277. .71355
                /note="GRAIL, score = 85.000%, comment = excellent"
                /evidence=not_experimental
exon            71277. .71355
                /note="MZEF, score = 77.8%"
                /evidence=not_experimental
repeat_region   complement(71530. .71824)
                /rpt_family="AluY"
                /evidence=not_experimental
exon            71935. .72064
                /note="GRAIL, score = 51.000%, comment = good"
                /evidence=not_experimental
exon            71982. .72064
                /note="MZEF, score = 73.4%"
                /evidence=not_experimental
repeat_region   72387. .72626
                /rpt_family="AluSg"
                /evidence=not_experimental
repeat_region   73051. .73267
                /rpt_family="L1ME"
                /evidence=not_experimental
exon            complement(74844. .74963)
```

```
                /note="GRAIL, score = 100.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(74844. .74963)
                /note="MZEF, score = 86.2%"
                /evidence=not_experimental
repeat_region   75339. .75640
                /rpt_family="AluSp"
                /evidence=not_experimental
exon            complement(75683. .75743)
                /note="GRAIL, score = 90.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(76645. .76667)
                /note="Xpound exon prediction, score = 67% (0%)"
                /evidence=not_experimental
repeat_region   complement(76870. .77169)
                /rpt_family="AluSg1"
                /evidence=not_experimental
exon            76893. .77032
                /note="MZEF, score = 64.8%"
                /evidence=not_experimental
exon            complement(77071. .77199)
                /note="MZEF, score = 81.3%"
                /evidence=not_experimental
exon            77812. .77923
                /note="MZEF, score = 61.3%"
                /evidence=not_experimental
exon            78090. .78218
                /note="GRAIL, score = 52.000%, comment = good shadow"
                /evidence=not_experimental
exon            79137. .79206
                /note="GRAIL, score = 59.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(79512. .79698)
                /rpt_family="MER5A"
                /evidence=not_experimental
repeat_region   79699. .79913
                /rpt_family="LTR16C"
                /evidence=not_experimental
repeat_region   79945. .80056
                /rpt_family="L2"
                /evidence=not_experimental
exon            complement(80382. .80511)
                /note="GRAIL, score = 52.000%, comment = good"
                /evidence=not_experimental
exon            complement(80382. .80511)
                /note="MZEF, score = 95%"
                /evidence=not_experimental
repeat_region   80408. .80552
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   80973. .81310
                /rpt_family="THE1B"
                /evidence=not_experimental
repeat_region   82003. .82480
                /rpt_family="L2"
                /evidence=not_experimental
exon            82065. .82284
                /note="MZEF, score = 76.8%"
                /evidence=not_experimental
repeat_region   complement(83070. .83895)
                /rpt_family="TIGGER1"
                /evidence=not_experimental
repeat_region   83897. .84197
                /rpt_family="AluSx"
                /evidence=not_experimental
repeat_region   complement(84212. .85874)
                /rpt_family="L1PA2"
                /evidence=not_experimental
exon            84288. .84322
                /note="GRAIL, score = 59.000%, comment = good shadow"
                /evidence=not_experimental
exon            complement(84395. .85492)
                /note="GRAIL, score = 81.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(84815. .84966)
                /note="MZEF, score = 52.8%"
                /evidence=not_experimental
exon            85572. .85679
                /note="GRAIL, score = 90.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            complement(85585. .85735)
                /note="GRAIL, score = 73.000%, comment = good"
                /evidence=not_experimental
exon            85589. .85623
                /note="Xpound exon prediction, score = 73% (0%)"
                /evidence=not_experimental
exon            complement(85810. .85841)
                /note="Xpound exon prediction, score = 74% (4%)"
                /evidence=not_experimental
repeat_region   85873. .86874
                /rpt_family="L1PA2"
                /evidence=not_experimental
exon            complement(86764. .86853)
                /note="MZEF, score = 55.3%"
                /evidence=not_experimental
repeat_region   complement(87244. .87505)
                /rpt_family="L1M4"
                /evidence=not_experimental
repeat_region   87776. .88330
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   88476. .88764
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   complement(88804. .88978)
                /rpt_family="MER5B"
                /evidence=not_experimental
repeat_region   complement(89035. .89144)
                /rpt_family="MER5B"
                /evidence=not_experimental
exon            complement(89293. .89397)
                /note="GRAIL, score = 87.000%, comment = excellent"
                /evidence=not_experimental
exon            90840. .91058
                /note="GRAIL, score = 90.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            90840. .91058
                /note="MZEF, score = 86.8%"
                /evidence=not_experimental
exon            complement(90870. .91148)
                /note="GRAIL, score = 100.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(90870. .91148)
                /note="MZEF, score = 79.1%"
                /evidence=not_experimental
exon            complement(90884. .91114)
                /note="Xpound exon prediction, score = 98% (0%)"
                /evidence=not_experimental
repeat_region   91620. .91924
                /rpt_family="AluJo"
                /evidence=not_experimental
repeat_region   complement(92814. .92927)
                /rpt_family="L2"
                /evidence=not_experimental
exon            92828. .93069
                /note="MZEF, score = 58.1%"
                /evidence=not_experimental
exon            92966. .93069
                /note="GRAIL, score = 71.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   93543. .93652
                /rpt_family="MIR"
                /evidence=not_experimental
exon            93807. .93863
                /note="MZEF, score = 94.9%"
                /evidence=not_experimental
```

```
repeat_region   93906. .94210
                /rpt_family="AluSx"
                /evidence=not_experimental
exon            95387. .95462
                /note="MZEF, score = 89.2%"
                /evidence=not_experimental
exon            complement(95496. .95596)
                /note="MZEF, score = 54.4%"
                /evidence=not_experimental
repeat_region   complement(96315. .96619)
                /rpt_family="AluSq"
                /evidence=not_experimental
repeat_region   complement(96735. .96868)
                /rpt_family="L1PA4"
                /evidence=not_experimental
repeat_region   96862. .97124
                /rpt_family="L1PA4"
                /evidence=not_experimental
repeat_region   complement(98239. .98562)
                /rpt_family="L1M3"
                /evidence=not_experimental
repeat_region   98620. .98996
                /rpt_family="L1PA10"
                /evidence=not_experimental
exon            98693. .98823
                /note="GRAIL, score = 89.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   complement(99313. .99682)
                /rpt_family="THE1B"
                /evidence=not_experimental
exon            complement(99916. .100033)
                /note="MZEF, score = 46.4%"
                /evidence=not_experimental
exon            complement(100874. .100955)
                /note="GRAIL, score = 61.000%, comment = good"
                /evidence=not_experimental
exon            100949. .101033
                /note="GRAIL, score = 71.000%, comment = good shadow"
                /evidence=not_experimental
repeat_region   complement(101311. .101613)
                /rpt_family="AluSq"
                /evidence=not_experimental
repeat_region   101701. .102079
                /rpt_family="LTR16A"
                /evidence=not_experimental
exon            complement(101953. .102007)
                /note="Xpound exon prediction, score = 62% (0%)"
                /evidence=not_experimental
exon            complement(101957. .102172)
                /note="GRAIL, score = 59.000%, comment = good"
                /evidence=not_experimental
repeat_region   102611. .102912
                /rpt_family="AluSq"
                /evidence=not_experimental
repeat_region   104460. .104688
                /rpt_family="L1MC/D"
                /evidence=not_experimental
exon            105198. .105306
                /note="GRAIL, score = 60.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(106166. .106598)
                /rpt_family="L1MA8"
                /evidence=not_experimental
repeat_region   106611. .108110
                /rpt_family="L1MA8"
                /evidence=not_experimental
repeat_region   108145. .108421
                /rpt_family="AluSc"
                /evidence=not_experimental
repeat_region   108484. .108936
                /rpt_family="L1MA8"
                /evidence=not_experimental
repeat_region   complement(112171. .112428)
                /rpt_family="AluSx"
                /evidence=not_experimental
repeat_region   complement(112545. .112687)
                /rpt_family="FRAM"
                /evidence=not_experimental
exon            complement(112720. .112773)
                /note="Xpound exon prediction, score = 83% (0%)"
                /evidence=not_experimental
repeat_region   112932. .113418
                /rpt_family="L2"
                /evidence=not_experimental
repeat_region   complement(113426. .113600)
                /rpt_family="FAM"
                /evidence=not_experimental
repeat_region   113608. .113972
                /rpt_family="L2"
                /evidence=not_experimental
exon            complement(113873. .114097)
                /note="MZEF, score = 47.8%"
                /evidence=not_experimental
repeat_region   114523. .115498
                /rpt_family="CHARLIE1a"
                /evidence=not_experimental
repeat_region   115524. .115686
                /rpt_family="L2"
                /evidence=not_experimental
exon            complement(116890. .117165)
                /note="GRAIL, score = 100.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(116890. .117165)
                /note="MZEF, score = 50.2%"
                /evidence=not_experimental
exon            complement(116890. .116985)
                /note="Xpound exon prediction, score = 99% (0%)"
                /evidence=not_experimental
exon            complement(117476. .117688)
                /note="GRAIL, score = 64.000%, comment = good"
                /evidence=not_experimental
exon            117535. .117693
                /note="GRAIL, score = 89.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            complement(117915. .118204)
                /note="MZEF, score = 65.7%"
                /evidence=not_experimental
exon            complement(117915. .118173)
                /note="GRAIL, score = 99.000%, comment = excellent"
                /evidence=not_experimental
exon            complement(117917. .118103)
                /note="Xpound exon prediction, score = 97% (0%)"
                /evidence=not_experimental
exon            117936. .118085
                /note="GRAIL, score = 78.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            complement(118249. .118332)
                /note="GRAIL, score = 87.000%, comment = excellent"
                /evidence=not_experimental
exon            118285. .118383
                /note="GRAIL, score = 93.000%, comment = excellent shadow"
                /evidence=not_experimental
exon            118350. .118383
                /note="Xpound exon prediction, score = 86% (0%)"
                /evidence=not_experimental
repeat_region   complement(118590. .118657)
                /rpt_family="MADE1"
                /evidence=not_experimental
repeat_region   complement(120240. .120488)
                /rpt_family="L1ME2"
                /evidence=not_experimental
repeat_region   complement(120508. .120867)
                /rpt_family="L1MC4"
                /evidence=not_experimental
exon            complement(120672. .120866)
                /note="GRAIL, score = 40.000%, comment = marginal"
```

```
                     /evidence=not_experimental
     repeat_region   complement(120846. .120949)
                     /rpt_family="L1M"
                     /evidence=not_experimental
BASE COUNT    36978 a  24540 c  24208 g  35293 t
ORIGIN
```

Query Match 4.7%; Score 307.2; DB 42; **Length 121019;**
Best Local Similarity 89.7%; Pred. No. 2.3e-48;
Matches 330; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```
Qy   1654 tccttgaagatggaactcccaaaattatttctgcctttagtgaaaaggtggtgagtccag 1713
          | | || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118213 TTCCTGCAGATGGAACTCCCAAAATTATTTCTGCCTTTAGTGAAAAGGTGGTGAGTCCAG 118154

Qy   1714 cagagccggtttcccttatgtgcaacgtgaagggaacacctttgcccacgatcacgtgga 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118153 CAGAGCCGGTTTCCCTTATGTGCAACGTGAAGGGAACACCTTTGCCCACGATCACGTGGA 118094

Qy   1774 ccctggacgatgacccgattctcaagggtggcagtcacccgcatcagccagatgatcacgt 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118093 CCCTGGACGATGACCCGATTCTCAAGGGTGGCAGTCACCGCATCAGCCAGATGATCACGT 118034

Qy   1834 cggaggggaacgtggtcagctacctgaacatctccagctcccaggtccgggacgggggag 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118033 CGGAGGGGAACGTGGTCAGCTACCTGAACATCTCCAGCTCCAGGTCCGGGACGGGGGAG 117974

Qy   1894 tctaccgctgcactgccaacaactcggcgggagtcgtcctgtaccaggctcgaataaacg 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 117973 TCTACCGCTGCACTGCCAACAACTCGGCGGGAGTCGTCCTGTACCAGGCTCGAATAAACG 117914

Qy   1954 taagagggcctgcaagcattcgaccaatgaaaaacatcacagcaatagcaggacgggaca 2013
          |||||||  ||      ||  |  |    |||||   ||||  | |      |  ||| |
Db 117913 TAAGAGGTGCTTGTCAAATCAGCTCCTCAAAAAAACACACATAACTCATTATAGTGGAGA 117854

Qy   2014 catacatt 2021
             | |||
Db 117853 AGAAGATT 117846
```

Search completed: July 23, 1999, 12:05:32
Job time: 4690 sec